## CLAIMS

1    1.    An apparatus comprising:

2    a sequence database configured to contain entries of sequences;

3    a sequence comparitor configured to receive a patient sample sequence, to

4    compare the patient sample sequence with entries in the sequence database

5    to determine closest matches, and to normalize a matching score of the

6    closest matches.

1    2.    The apparatus of claim A1, wherein the sequence comparitor is further

2    configured to determine whether the matching score of the closest matches

3    are within a confidence threshold.

1    3.    The apparatus of claim A2 further comprising:

2    a patient profile manager to reporting whether a sample patient identifier

3    associated with the patient sample sequence matches a matched patient

'4   identifier associated with the closest match;

1    4.    The apparatus of claim A3 wherein the patient sample sequence is

2    sequenced from a virus.

1    5.    The apparatus of claim A4 wherein the virus is hepatitis or Human

2    Immunodeficiency Virus (HIV).

1    6.    The apparatus of claim A3 wherein the patient sample sequence is

2    sequenced from deoxyribonucleic acid (DNA).

1    7.    The apparatus of claim A5 wherein the confidence threshold is

2    approximately three standard deviations from an average normalized

3    score.

1    8.    A method comprising:

2       receiving a patient sample sequence, the patient sample sequence being associated

3           with a sample patient identifier;

4       comparing the patient sample sequence with entries in a sequence database to

5           determine closest matches, the closest matches being associated with a

6           matched patient identifier;

7       normalizing a matching score of the closest matches.

1       9.      The method of claim 8 further comprising:

2       determining whether the matching score of the closest matches are within a

3           confidence threshold.

1       10.      The method of claim 9 further comprising:

2       reporting the closest matches within the confidence threshold.

1       11.      The method of claim 9 further comprising:

2       reporting whether the sample patient identifier matches the matched patient

3           identifier;

1       12.      The method of claim 11 wherein the patient sample sequence is sequenced

2           from a virus.

1       13.      The method of claim 12 wherein the virus is hepatitis or Human

2           Immunodeficiency Virus (HIV).

1       14.      The method of claim 10 wherein the patient sample sequence is sequenced

2           from deoxyribonucleic acid (DNA).

1       15.      The method of claim 13 wherein the confidence threshold is approximately

2           three standard deviations from an average normalized score.

1       16.      A computer-readable medium encoded with data and instructions, the data

2           and instructions causing an apparatus executing the instructions to:

3    receive a patient sample sequence, the patient sample sequence being associated

4        with a sample patient identifier;

5    compare the patient sample sequence with entries in a sequence database to

6        determine closest matches, the closest matches being associated with a

7        matched patient identifier;

8    normalize a matching score of the closest matches.

1    17.    The computer-readable medium of claim 16 wherein the instruction further

2        causes an apparatus to:

3    determine whether the matching score of the closest matches are within a

4        confidence threshold.

1    18.    The computer-readable medium of claim 17 wherein the instruction further

2        causes an apparatus to:

3    report the closest matches within the confidence threshold.

1    19.    The computer-readable medium of claim 18 wherein the instruction further

2        causes an apparatus to:

3    report whether the sample patient identifier matches the matched patient identifier.

1    20.    The computer-readable medium of claim 19 wherein the patient sample

2        sequence is sequenced from a virus.

1    21.    The computer-readable medium of claim 20 wherein the virus is hepatitis

2        or Human Immunodeficiency Virus (HIV).

1    22.    The computer-readable medium of claim 18 wherein the patient sample

2        sequence is sequenced from deoxyribonucleic acid (DNA).

1    23.    The computer-readable medium of claim 21 wherein the confidence

2        threshold is approximately three standard deviations from an average

3        normalized score.

1    24.    An apparatus comprising:

2    means for receiving a patient sample sequence, the patient sample sequence being

3           associated with a sample patient identifier;

4    means for comparing the patient sample sequence with entries in a sequence

5           database to determine closest matches, the closest matches being

6           associated with a matched patient identifier;

7    means for normalizing a matching score of the closest matches.

1    25.    The apparatus of claim 24 further comprising:

2    means for determining whether the matching score of the closest matches are

3           within a confidence threshold.

1    26.    The apparatus of claim 25 further comprising:

2    means for reporting the closest matches within the confidence threshold.

1    27.    The apparatus of claim 26 further comprising:

2    means for reporting whether the sample patient identifier matches the matched

3           patient identifier;

1    28.    The apparatus of claim 27 wherein the patient sample sequence is

2           sequenced from a virus.

1    29.    The apparatus of claim 28 wherein the virus is hepatitis or Human

2           Immunodeficiency Virus (HIV).

1    30.    The apparatus of claim 26 wherein the patient sample sequence is

2           sequenced from deoxyribonucleic acid (DNA).

1    31.    The apparatus of claim 29 wherein the confidence threshold is

2           approximately three standard deviations from an average normalized

3           score.